



Blast 2 Sequences results

PubMed

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OMIM

Taxonomy

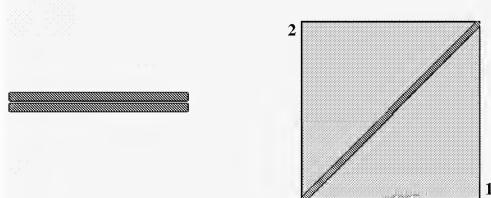
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **0** expect: **10.00** wordsize: **3** Filter ☒ View option: **Standard**
 Masking character option: **X for protein, n for nucleot** Masking color option: **Black**
☐ Show CDS translation **Align**

Sequence 1: gi|6706916|spike glycoprotein [bovine coronavirus] Genbank Accession# AAF25499
 Length = 1363 (1 .. 1363)

Sequence 2: unnamed protein product SEQ ID NO: 4
 Length = 1363 (1 .. 1363)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 2625 bits (6803), Expect = 0.0

Identities = 1311/1363 (96%), Positives = 1337/1363 (98%), Gaps = 0/1363 (0%)

Query	1	MFLILLISLPMALAVIGDLKCTTVSINDVDTGVPVSVDSTDVDVTNGLGTYTVLDRVYLN	60
Sbjct	1	MFLILLISLPMALAVIGDLKCTTVSINDVDTG PS+STD VDVVTNGLGTYTVLDRVYLN	60
Query	61	TLLNGYYPTSGSTYRNMAKGTLLSTLWFKPPFLSDFINGIFAKVKNTKVIKNGVMYS	120
Sbjct	61	TLLNGYYPTSGSTYRNMAKGTLLSTLWFKPPFLSDFI+G+FAKVKNTKVIK+GV+YS	120
Query	121	EFPAITIGSTFVNNTSYSVVVQPHTTNLDNKLQGLLEISVCQYTMCEYPHTICHPNLGNRR	180

		EFPAITIGSTFVNTSYSVVVQPHHTNLNDKQLGLLEISVCQYTM+CYPHT+CHPNLGN+R	
Sbjct	121	EFPAITIGSTFVNTSYSVVVQPHHTNLNDKQLGLLEISVCQYTMCDYPHTMCHPNLGNKR	180
Query	181	IELWHWDTGVSCLYKRNFYTDVNADYLYHFHYQEGGTFYAYFTDTGVVTKFLFNVLGT	240
		IELWHWDTGVS CLYKRNFYTDVNADYLY HFYQEGGTFYAYFTDTGVVTKFLF+VVLGT	
Sbjct	181	IELWHWDTGVSCLYKRNFYTDVNADYLYSHFYQEGGTFYAYFTDTGVVTKFLFHVVLGT	240
Query	241	VLSHYYVMPLTCSAMTLEYWVTPLTSKQYLLAFNQDGVIFNAVDCKSDFMSEIKCKTSL	300
		VLSHYYVMPLTCSAMTLEYWVTPLT KQYLLAFNQDGVIFNAVDCKSDFMSEIKCKTSL	
Sbjct	241	VLSHYYVMPLTCSAMTLEYWVTPLTFKQYLLAFNQDGVIFNAVDCKSDFMSEIKCKTSL	300
Query	301	IAPSTGVYELNGYTVQPIADVRRIPNLPCNIEAWLNDKSVSPNLNWERKTFSCNCFNM	360
		IAPSTGVYELNGYTVQPIADVRRIPNLPCNIEAWLNDKSVSPNLNWERKTFSCNCFNM	
Sbjct	301	IAPSTGVYELNGYTVQPIADVRRIPNLPCNIEAWLNDKSVSPNLNWERKTFSCNCFNM	360
Query	361	SSLMSFIQADSFCTNNIDAAKIYGMCFSSITIDKFAIPNGRKVDLQGLNGLYQSFNYRI	420
		SSLMSFIQADSFCTNNIDAAKIYGMCF SITIDKFAIPNGRKVDLQ+GNLGLYQSFNYRI	
Sbjct	361	SSLMSFIQADSFCTNNIDAAKIYGMCFSSITIDKFAIPNGRKVDLQMGNLGLYQSFNYRI	420
Query	421	DTTATSCQLYYNLPAAVSVSRFNPSTWNRFGFTEQSVFKPQPVGVFTDHDVVYAQHCF	480
		DTTATSCQLYYNLPAAVSVSRFNPST WNRFGFTEQSVFKPQPVGVFTDHDVVYAQHCF	
Sbjct	421	DTTATSCQLYYNLPASVSVSRFNPSTWNRFGFTEQSVFKPQPVGVFTDHDVVYAQHCF	480
Query	481	KAPTNCPCCKLDGSLCVGSGSIDAGYKNSGIGTCAGTNYLTCHNAAQCNCCLCTPDPI	540
		KAPTNCPCCKL+GSLCVGSG SIDAGYKNSGIGTCAGTNYLTCHNAAQCNCCLCTPDPI	
Sbjct	481	KAPTNCPCCKLNGSLCVGSGSIDAGYKNSGIGTCAGTNYLTCHNAAQCNCCLCTPDPI	540
Query	541	SKSTGPYKCPQTKYLVGIGEHCGLAIKSDYCGGNPCTCQPAFLGWSVDSCLQGDRONI	600
		SKSTGPYKCPQTKYLVGIGEHCGLAIKSDYCGGNPCTCQPAFLGWSVDSCLQGDRONI	
Sbjct	541	SKSTGPYKCPQTKYLVGIGEHCGLAIKSDYCGGNPCTCQPAFLGWSVDSCLQGDRONI	600
Query	601	FANFILHDVNSGTTCTSDLQKSNITDILGVCVNYDLYGITGQIFVEVNATYYNSWQNL	660
		FANFILH VNSGTTCTSDLQKSNITDILGVCVNYDLYGITGQIFVEVNATYYNSWQNL	
Sbjct	601	FANFILHGVNSGTTCTSDLQKSNITDILGVCVNYDLYGITGQIFVEVNATYYNSWQNL	660
Query	661	YDSNGNLYGFRDYLNTNRTFMIRSCYSGRVSAFHSNSSEPALLFRNIKCNVFNNTLSRQ	720
		YDSNGNLYGFRDYLNTNRTFMIRSCYSGRVSA FH+NSSEPALLFRNIKCNVFNNTLSRQ	
Sbjct	661	YDSNGNLYGFRDYLNTNRTFMIRSCYSGRVSAFHSNSSEPALLFRNIKCNVFNNTLSRQ	720
Query	721	LQPINYFDSYLGCVVNADNSTSSAVQTCDLTVGSGYCDYSTKRRSRRAITTYGFRFTNFE	780
		LQPINYFDSYLGCVVNADNSTSS+VQTCDLTVGSGY DYST+RRSRRAITTYGFRFTNFE	
Sbjct	721	LQPINYFDSYLGCVVNADNSTSSVQTCDLTVGSGYWDYSTKRRSRRAITTYGFRFTNFE	780
Query	781	PFTVNSVNDLSLEPVGGLEYEIQIPSEFTIGNMEEFIQISSPKVTIDCSAFVCGDYAACKSQ	840
		PFTVN VNDL PVGGLEYEIQIPSEFTIGNMEEFIQ SPKVTIDC FVCGDYAACKSQ	
Sbjct	781	PFTVNPVNDLSLHPVGGLEYEIQIPSEFTIGNMEEFIQTRSPKVTIDCPVFVCGDYAACKSQ	840
Query	841	LVEYGSFCDNINAILTEVNELLDTTQLQVANSLSMNGVTLSKTKLDGVNFNVDDINFSPVL	900

		LVEYGSFCDNINAILTEVNELLDTTQLQVANSLSMNGVTLSKCLKDG NFNVDDINFSPVL	
Sbjct	841	LVEYGSFCDNINAILTEVNELLDTTQLQVANSLSMNGVTLSKCLKDGFNFNVDDINFSPVL	900
Query	901	GCLGSDCNKVSSRSAIEDLLFSKVKLSDVGFVEAYNNCTGGAEIRDLICVQSYNGIKVLP	960
		GCLGS+CNKVSSRSAIEDLLFSKVKLSDVGFV+AYNNCTGGAEIRDLICVQSYNGIKVLP	
Sbjct	901	GCLGSECNKVSSRSAIEDLLFSKVKLSDVGFVDAYNNCTGGAEIRDLICVQSYNGIKVLP	960
Query	961	PLLSENQISGYTLAATSASLFPWWSAAAGVPFYLVNQYRINGIGVTMDVLSQNQKLIANA	1020
		PLLSENQISGYTLAAT ASLFPWWSAAAGVPFYLVNQYRINGIGVTMDVL+QNQKLI+NA	
Sbjct	961	PLLSENQISGYTLAATFASLFPWWSAAAGVPFYLVNQYRINGIGVTMDVLTQNQKLISNA	1020
Query	1021	FNNALDAIQEGFDATNSALVKIQAVVNANAEALNNLLQQLSNRFGAISSSLQEILSRLDA	1080
		FNNALDAIQEGFDATNSALVKIQAVVNANAEALNNLLQQLSN+FGAIS+SLQEILSRLDA	
Sbjct	1021	FNNALDAIQEGFDATNSALVKIQAVVNANAEALNNLLQQLSNKFGAISASLQEILSRLDA	1080
Query	1081	LEAQAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNECVKSQSSRINF CGNG	1140
		LEAQAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNECVKSQSSRINF CGNG	
Sbjct	1081	LEAQAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMEKVNECVKSQSSRINF CGNG	1140
Query	1141	NHIIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVTWMT	1200
		NHIIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVTWMT	
Sbjct	1141	NHIIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVTWMT	1200
Query	1201	GSYYYYPEPITGNVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQTSVAPD	1260
		GSYYYYPEPITGNVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQTSVAPD	
Sbjct	1201	GSYYYYPEPITGNVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQTLMAPD	1260
Query	1261	LSLDYINVTFLDLQDEMNRLQEAIKVLNQSYINLKDIGTYEYVVKWPWYVWLLIGLAGVA	1320
		LSLDYINVTFLDLQDEMNRLQEAIKVLN SYINLKDIGTYEYVVKWPWYVWLLIGLAGVA	
Sbjct	1261	LSLDYINVTFLDLQDEMNRLQEAIKVLNHSYINLKDIGTYEYVVKWPWYVWLLIGLAGVA	1320
Query	1321	MLVLLFFICCTGCGTSCFKKCGGCCDDYTGHQELVIKTSHDD	1363
		MLVLLFFICCTGCGTSCFKKCGGCCDDYTGHQELVIKTSHDD	
Sbjct	1321	MLVLLFFICCTGCGTSCFKKCGGCCDDYTGHQELVIKTSHDD	1363

CPU time: 0.05 user secs. 0.03 sys. secs 0.08 total secs.